

SEQUENCE ANNEX 1a - Complete genomic sequence of EHV-1 strain V592

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SEQUENCE ANNEX 1b - EHV-1 strain V592 feature table

FEATURES	Location/Qualifiers
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primase"

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 CDS complement(47337..48164)
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 probable interaction with pORF29"
 /note="homologous to HSV-1 UL34"
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 /product="membrane associated phosphoprotein"
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 gene complement(48303..48725)
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 CDS complement(48303..48725)
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        /function="role in DNA packaging"
        /note="ORF27; homologous to HSV-1 UL33"
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        48697..51532
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        CDS      48697..50559
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        /function="role in DNA packaging"
        /note="homologous to HSV-1 UL32"
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        50552..51532
        /gene="EHV-1 ORF28"
        /function="probable interaction with pORF26, role in
        envelopment at nuclear membrane"
        /note="homologous to HSV-1 UL31"
        /codon_start=1
        /product="putative product of ORF29"

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        complement(51456..55118)
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        CDS      complement(51456..55118)
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      /gene="EHV-1 ORF31"
      CDS      55387..59016
      /gene="EHV-1 ORF31"
      /note="homologous to HSV-1 UL29"
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gene	59177..61504
	/gene="EHV-1 ORF32"
CDS	59177..61504
	/gene="EHV-1 ORF32"
	/function="role in DNA packaging, probable interaction with pORF28"
	/note="homologous to HSV-1 UL28"
	/codon_start=1
	/product="putative product of ORF32"

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 RRLECTCDHITRQMAVRVANIDIARHLPHALSVASERRAAAEALRALEARRVQGHN
 GKSAGTEDPTQQVASRLLESHHVFKPASRCLYAVSELKFWLASTKHGDMGQPRAIDTF
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 /gene="EHV-1 ORF33"
 CDS 61366..64308
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 /function="role in virus binding/entry"
 /note="homologous to HSV-1 UL27"
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 CDS 64512..64994
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 /note="homologous to VZV gene 32"
 /codon_start=1
 /product="putative product of ORF34"

/translation="MDSPRGISTATGDAHAEAAVSPAAEIQIKTEAPDVGPEATTEC
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gene complement(65087..66076)
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gene complement(65087..67027)
/gene="EHV-1 ORF35"
CDS complement(65087..66076)
/gene="EHV-1 ORF35.5"
/note="homologous to HSV-1 UL26.5"
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/product="major capsid scaffold protein"

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CDS complement(65087..67027)
/gene="EHV-1 ORF35"
/function="capsid maturation and scaffold activities"
/note="homologous to HSV-1 UL26"
/codon_start=1
/product="capsid protein"

/translation="MDAYTVDGNAVSLPIYVAGYIALYDMGDGGELTLTRETVAALP
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gene complement(67146..68909)
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CDS complement(67146..68909)
/gene="EHV-1 ORF36"
/function="role in DNA packaging"

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        /function="putative virulence determinant"
        /note="homologous to HSV-1 UL24"
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        /gene="EHV-1 ORF38"
        CDS        69843..70901
        /gene="EHV-1 ORF38"
        /note="homologous to HSV-1 UL23"
        /codon_start=1
        /product="thymidine kinase"

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gene      71125..73671
          /gene="EHV-1 ORF39"
CDS       71125..73671
          /gene="EHV-1 ORF39"
          /function="virus entry, interacts with gL"
          /note="homologous to HSV-1 UL22"
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          /product="envelope glycoprotein H (gH)"

/translation="MLQPYRKMLIFAVVTVAFAFAMAVWSTPVPATPSGVGNATWANNSE
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gene 76726..77445
 /gene="EHV-1 ORF41"

CDS 76726..77445
 /gene="EHV-1 ORF41"
 /function="role in virion egress, probable interaction
 with gK"
 /note="homologous to HSV-1 UL20"
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/translation="MPQVLMGNTRLHAPLEDGIPLIENDENSSEQNEVDLYDYVSMSSY
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gene 77636..81766
 /gene="EHV-1 ORF42"

CDS 77636..81766
 /gene="EHV-1 ORF42"
 /note="homologous to HSV-1 UL19"
 /codon_start=1
 /product="major capsid protein"

/translation="MDRRSEAFKIPVPEVIPAGQILSTIEVSSHRTLFDFFKQIRSD
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gene 82016..82960
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CDS 82016..82960
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IPNLLTLGTQDGFVNAAIQMGSATREVGQLVHQQPVPQPQDGARRFCVYDALMSWISV
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gene complement(83081..88850)
/gene="EHV-1 ORF44_47 (spliced)"
CDS complement(join(83081..84253,87819..88850))
/gene="EHV-1 ORF44_47 (spliced)"
/function="probable interaction with pORF32"
/note="homologous to HSV-1 UL15"
/codon_start=1
/product="putative terminase"

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VARFSRLVDTSFNGADLDGDGQQASKRARVDVPTYGKQRGTLLELFQKMILMHATYFIA
AVILGDHADRIGAFLLKMFNTPEFSDATIRHFRQRATVFLVPRRHGKTWFLVPLIALA
LATEFKGIKIGYTAHIRKATEPVFDEIGARLRQWFGNSPVDHVKGENISFSFPDGSKST
IVFASSHNTNGIRGQDFNLLFVDEANFIRPEAVQTIIGFLNQTNCKIIFVSSTNTGKA
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TAEFLPDSFMQEIIIGGGNVSGAHRDEPVFTKTAQDRFLLYRPSTVANQDIMSSDLYV
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 /gene="EHV-1 ORF45"
 CDS 84413..86533
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 /note="homologous to HSV-1 UL17"
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 RRQCVASGLRQGARGAHASDSHARVGFNSSIHDATAALLGLEPPDSGRFVNSSGPQRHL
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 LSHLNILSGNKRGRLPYHRSWLPVSLAGGADAFLEFDYSSSGGEVVKVSPVPLAILVTAT
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 gene 86553..87665
 /gene="EHV-1 ORF46"
 CDS 86553..87665
 /gene="EHV-1 ORF46"
 /note="homologous to HSV-1 UL16"
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 /product="tegument protein"
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 DRLDVSNFATPAQPPKDKYDCCVLAPGVWWSNANKAIYFLQMDVALLALCPAGWKARG
 LGIILGRLLNHQEGCATCRFTEHSDPLNATADSVATPESCLCWAPCLWRKAHQRELT
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gene      88880..89833
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CDS       88880..89833
          /gene="EHV-1 ORF48"
          /note="homologous to HSV-1 UL14"
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          /product="probable tegument protein"

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RVSTRIAADPHSPRSTCPAPRKAPEDARCARKPGEVNNYTPSAQPRSQETTVDHLAS
PDEGTRLGDRTRDLEHHSTAPMRTHPNVLASERRRLGVVHQREKSSESQESATRSKAI
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gene      89302..91086
          /gene="EHV-1 ORF49"
CDS       89302..91086
          /gene="EHV-1 ORF49"
          /function="serine/threonine protein kinase"
          /note="homologous to HSV-1 UL13"
          /codon_start=1
          /product="tegument protein"

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NSDNERSHLPRLSSHGVVRVGGRLPTQTPLQKTIILQPKLVRKVFMPFTFTVNPEMHYR
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DLYALGQALLELLLVCISPCLSVPILRATATYYYYSNKLSVDYALDLLAYRCSLYPAL
FPTTPLTTIYGIPWDQVEGVFESIAGAAHREAFRAHLERYRLTHRRLFASIRIPSAFT
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gene      91068..92765
          /gene="EHV-1 ORF50"
CDS       91068..92765
          /gene="EHV-1 ORF50"
          /note="homologous to HSV-1 UL12"
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GLLMDARTGVVGASLDMLVCDRDPGVLSPHSTQTTLDFFEIKCRAKYLFDPDLFSPV
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    gene          92717..92941
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    CDS           92717..92941
                  /gene="EHV-1 ORF51"
                  /note="homologous to HSV-1 UL11"
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                  /product="tegument protein"

/translation="MGQRLSCGCFRTDQLVTHSGEVVSLNADTFEEFSMEEFDIPPPP
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    gene          complement(93053..94405)
                  /gene="EHV-1 ORF52"
    CDS           complement(93053..94405)
                  /gene="EHV-1 ORF52"
                  /function="role in envelope fusion, interaction with gN"
                  /note="homologous to HSV-1 UL10"
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                  /product="envelope glycoprotein M (gM)"

/translation="MARRGA AVAE EPLL PSSGIVGIGPIEGINWRTWLVQVFCFALTT
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VAFLYYTTLVLVAISFYLIISAVLVRRYARGKECTAVAGCTRPTTTLIASHVTLLVLT
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    gene          94323..96986
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    CDS           94323..96986
                  /gene="EHV-1 ORF53"
                  /function="helicase"
                  /note="homologous to HSV-1 UL9"
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                  /product="origin binding protein"

/translation="MPSIGPIPTIPDEGSRGSSATAAPRRAMASYRDTTLGGRAEGVA
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 VRGVTTALSGRPKSRVPLSKGEHAVSLFKVLWEDVFGAKLAKSTQTFPGGVRVKNLRK
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 gene 97002..99257
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 CDS 97002..99257
 /gene="EHV-1 ORF54"
 /note="homologous to HSV-1 UL8"
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 LHQS
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gene      complement(99352..100263)
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CDS       complement(99352..100263)
          /gene="EHV-1 ORF55"
          /note="homologous to HSV-1 UL7"
          /codon_start=1
          /product="putative product ORF55"

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NYMMAKMLLGQKSNTPAILDAIYSAGYRQTL SKRPITPCPSGVLRCNKAHLNAPLCTK
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gene      complement(100061..102322)
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CDS       complement(100061..102322)
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          /note="homologous to HSV-1 UL6"
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gene      102306..104951
          /gene="EHV-1 ORF57"
CDS       102306..104951
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          /function="helicase"
          /note="homologous to HSV-1 UL5"
          /codon_start=1
          /product="component of helicase-primase complex"

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 AYKSPQYAEKGVPVIVCVGSPTQTDLESRFEHKNLKCHVRSSENVLTHIITNRTIRE
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CDS	105001..105678
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	/note="homologous to HSV-1 UL4"
	/codon_start=1
	/product="putative product of ORF58"

/translation="METCSPPVTFITYALYGIKTSPAWTLPNFEQVICSCDWGYRLIA
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 PCLSNND"

gene	complement(105808..106347)
	/gene="EHV-1 ORF59"
CDS	complement(105808..106347)
	/gene="EHV-1 ORF59"
	/note="positional homologue to VZV gene 57"
	/codon_start=1
	/product="putative product of ORF59"

/translation="MDVFGRGRAATADDYRRFLERNRRAAKLAAATTPHTASSRQQ
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gene      complement(106409..107047)
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CDS       complement(106409..107047)
          /gene="EHV-1 ORF60"
          /note="homologous to HSV-1 UL3"
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          /product="putative product of ORF60"

/translation="MESALTVLSGWGPVEVVTGPVADHLTEMPPAPTGTTCCTTTST
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SVIQARKPRKYYTRSSDGRTHPVVPVYTYEFSAVDKVYLHRDNVIEADAQAK"
gene      complement(107137..108075)
          /gene="EHV-1 ORF61"
CDS       complement(107137..108075)
          /gene="EHV-1 ORF61"
          /note="homologous to HSV-1 UL2"
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/translation="MSSACDHETEASHVNIPETTPPEENGSSNSTPTSEIGPACVVSPA
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GQAHGLAFSVRKGVPPPSLRNIYSAVQKSYPSFRHPMHGFLERWAEQGVLLINTTLT
VARGKPGSHATLGWHRLVRAVIDRLCTTSQGLVFMWGAHAQKSCSPNRQHHLVLTYG
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gene      complement(108078..108734)
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CDS       complement(108078..108734)
          /gene="EHV-1 ORF62"
          /function="role in virus entry, interaction with gL"
          /note="homologous to HSV-1 UL1"
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          /product="envelope glycoprotein H (gH)"

/translation="MYQILIGCVWQKSPYINQCTEFQPPLSFVTPERMRRFMRCWARL
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CDS       complement(110353..111951)
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          /note="homologous to HSV-1 RL2"
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/translation="MATVAERCPICLEDPSNYSMALPCLHAFCYVCITRWIRQNPTCP

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repeat_region 112316..112419
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 misc_feature 113013..113068
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AB4:AATGACGTCACCGGAAGGGGAGGAGCAGGAAATGACGTAGGCGGTAGTGACGTA
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repeat_region 113045..113089
 /note="novel repeat not present in AB4"
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 repeat_region 113358..113501
 /note="12 copies in V592 compared with 37 in AB4"
 /rpt_unit=CCATCAACCCGC
 gene 113835..148482
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 CDS complement(113835..118298)
 /note="homologous to HSV-1 RS1"
 /codon_start=1
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/translation="MASQRSDFAPDLYDFIESNDFGEDPLIRAASAAEEGFTQPAAPD
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 DEGGEETPRPRHSQNAAKTPSAAGSPGPSSGGDRPAAGAATPKSCRSGAASPGAPAP
 APASAPAPSRPGGGLLPPGARILEYLEGVREANLAKTLERPEPPAGMASPPGRSPHRL
 PKDQRPKSALAGASKRKRRANPRPIPQTQTQAPAEAPQTAVWDLDMNSSQATGAAAA
 AASAPAAASCAPGVYQREPLLTSPGDPWPGSDPPPMGRVRYGGTGDSRDGLWDDPEIV
 LAASRYAEAQAPVPVFPVPEMGDSTKQYNALVRMVFESEAMSRLQNSKLSGQDQNLAQ
 FCQKFIHAPRGHGSFITGSVANPLPHIGDAMAAGNALWALPHAAASVAMSRRYDRTQK
 SFILQSLRRAYADMAYPRDEAGRPDSLAAVAGYPAQAAAAAASQQQPEAPAPSVRVRE

AYTRVCAALGPRRKAAAAAAPGSRAPRPSAFRLRELGDACVLACQAVFEALLRLRG
 ASAVPGLDPSEIPSPACPPPEALCSNPAGLETAALSLYELRDLVERARLLGDSDPHRL
 GSDELRLAVRAVLVVARTVAPLVRYNAEGARARASAWTVTQAVFSIPSLVGGMLGEAV
 SLLAPPTRSQQPSSSSPGGEFFSGSAAAEGLQTLPLWPTVPGKQSATVPSSHSQSP
 QHSQSGGGAGATTATCCRATQTNARSRGQQHQPKARSPQAAAAPAHLSQEAMPGSSS
 DDRAIHGRPRGKSGKRRSEPLEPAAQAGASASFSSSARGYDPSGPVDSPPAPKRRVAT
 PGHQAPRALGMPAEGPDRRGFRVPRGDCHTPRPSDAACAAAYCPPELVAELIDNQL
 FPEAWRPALTFDPQALATIAARCSGPPARDGARFGELAASGPLRRRAAWMHQIPDPED
 VKVVVLYSPLQDEDLGGLPASRPGGSRREPLWSDLKGGLSALLAALGNRIILTKRSHA
 WAGNWTGAPDVSAALNAQGVLLLSTGDLAFTGCVEYLCRLGSAARRKLLVLDAVSTEDW
 PQDGPASISQYHIYMRAALTFRVACAVRWPRERHLSRAVLTSSTLFGPGLFARAEAAFA
 RLYPDSAPLRLCRSSNVAYTVDTRAGERTRVPLAPREYRQRVLPDYDGCKDMRAQAE
 LGFHDPDFEEGAAQSHRAANRWGLGAWLRPVYLACGRRGAGAVEPSELLIPELLSEFC
 RVALLEPDAAEPLVLPITEAPRRRAPRVWEPGFGSRSTSVLHMGATELCLPEPDDE
 LEIDGAGDVELVVEHPGSPGVAQALRRAPIKIEVVSDDEDGGDWCNPYLS"
 repeat_region 120814..120883
 /note="10 copies in V592 compared with 16 copies in AB4"
 /rpt_unit=GGTGGTC
 repeat_region 120955..121079
 /note="5 copies in V592 compared with 3 copies in AB4"
 /rpt_unit=CCCAGCTCCGGCGACCCCGGCCAG
 gene 121082..141235
 /gene="EHV-1 ORF65"
 CDS 121082..121963
 /gene="EHV-1 ORF65"
 /function="putative host range determinant"
 /note="homologous to HSV-1 US1"
 /codon_start=1
 /product="putative product of ORF65"
 /translation="MPHGQPCGACDGSRCMAQRGTPSTSPLIPSLTPSPAGDPSPRS
 SQRIDAVRVPARLPGGSDHPEYGMPLSPRALRPYLARGPGAFCAPPWRPDVNRLAGDV
 NRLFRGISTSSIHVTEDSRTLRRALLDFYAMGYTHTRPTLECWQSLQLLPEQSFPLR
 ATLRLNSEDRIEQRFLPEPPSDPPNTLFGEECDVSGDESPSEEEEEDEASGESSVSEF
 SPEEETASSEYDSFSDVGEDDSSCTGKWSSSESESDSESADPTNNHPTTRASAAKKR
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 gene 122581..139736
 /gene="EHV-1 ORF66"
 CDS 122581..123291
 /gene="EHV-1 ORF66"
 /note="homologous to HSV-1 US10"
 /codon_start=1
 /product="virion protein"

/translation="MDGAYGHVHNGSPMAVDGEESGAGTGTGAGADGLYPTSTDAAH
 AVSLPRSVGDFAAVVRAVSAEADALRSGAGPPAEAWPRVYRMFCDMFGRYAASPMPV
 FHSADPLRRRAVGRYLVDLGAAPVETHAELSGRMLFCAYWCCLGHAFACSRPQMYERAC

ARFFETRLGIGETPPADAERYWAALLNMAGAEPELFPRHAAAAAYLRARGRKLPLQLP
 SAHRTAKTVAVTGQSINF"
 repeat_region 123549..123656
 /note="variable copy number in V592"
 /rpt_unit=AGGCCGAGCGGGGAGAGCGGTAGGGG
 gene 123853..138464
 /gene="EHV-1 ORF67"
 CDS complement(123853..124671)
 /note="virulence determinant"
 /codon_start=1
 /product="product of ORF67 (IR6)"

/translation="MNSDMMTAATAGTEVFRICALARRRNANPPHLVLAPTFAAAAAGG
 AANSSGEEAPRGERKHLFNPFGCMLGRSYFRRCREEMNEGYFAKVPTGYFPVAPSEVP
 CRVPVEGVVAGEVLSYSALPLPKIEKRFYKQLNDGTFVRLPFLYPEVYYEGEEEPAD

RYYIRADAADASSADPSTLPEEAFKVPPIAIEGITNWQGPKRIPISERYVMKLGFE
 YQLHVTEDAFQEVNTSEFMRLDLQSSPDHPRGARQPRSAHVFAENPEDTPVAV"
 gene complement(124839..125750)
 /gene="EHV-1 ORF68"
 CDS complement(124839..125750)
 /gene="EHV-1 ORF68"
 /function="virulence factor"
 /note="homologous to HSV-1 US2, truncated via framshift
 compared with EHV-1 strain AB4"
 /codon_start=1
 /product="virion membrane protein"

/translation="MGVVLITVTVVDRHKALPNSSIDVDGHLWEFLSRQCFVLASEP
 LGIPIVVRADLYRFSSSLTLTPKACRPVIRTRGATAIALDRNGVVYHEDRMGVSIEW
 LSVLSGYNHLNSSLIIINQPYHLWVLGAADLCKPVFDLIPGPKRMVYAEIADEFHKSWQ
 PPFVCGKLFETIPWTTVEHNNHPLKLRAAGGEDTVVGECGFSKHSSNSLVHPPTVKRVI

YAVVDPARLREIPAPGRPLPRRRPSEGGMRAPRWRSRAPAPARSTAAAATPPRPGDPR
 APAARRAGDVTWMERLLWGVFGRTSTR"
 gene 125886..127034
 /gene="EHV-1 ORF69"
 CDS 125886..127034
 /gene="EHV-1 ORF69"
 /note="homologous to HSV-1 US3"
 /codon_start=1
 /product="serine-threonine protein kinase"

/translation="MENKQCDHLTDWFSTTSDASESMDTTPPLPPPTPSVDPSYSGAA
 ADEDLYSDISEGDLEYSDCDSASESDEDDDDCLIPSKEKAREVAASFGYTVIKTLTPG
 SEGRVMVATKDGQPEPVVLKIGQKGTTLIEAMMLRNVNHPSVIQMKDTLVSGAITCMV

LPHYSSDLYFTLTKESTRRIPIDQALIIEKQILEGLRYLHAQRIIHRDVKTENIFINSV
 DQVCIADFGAAQFPVVEPADLGLAGTVETNAPEVLARAKYNSKADIWSAGIVLFEMLA
 YPSTLFEDPPSTPEEYVKSCHSQQLLKIISTLKINPEEFPRDPGSRLVRGYIEYSRLER
 KPYTRYPCFQRVNLHIDGEFLVHKMLAFNAAMRPSAEELLSYPMFAQL"
 gene 127156..128391
 /gene="EHV-1 ORF70"
 CDS 127156..128391
 /gene="EHV-1 ORF70"
 /note="homologous to HSV-1 US4"
 /codon_start=1
 /product="envelope glycoprotein G (gG)"
 /translation="MLTVLAALSLLSLLTSATGRLAPDELCYAEPRRTGSPNTQPER
 PPVIFEPPTIAIKAESKGCELILLDPPIDVSYRREDKVNASIAWFFDFGACRMPIAYR
 EYYGCIGNAVPSPETCDAYSFTLIRTEGIVEFTIVNMSLLFQPGIYDSGNFIYSVLLD
 YHIFTGRVTLEVEKDTNYPGMIHGLTAYGNINVDETMDNASPHPRAVGCFPEPIDNE
 AWANVTFTTELGIPTDPSFLDDEGDYPNISDCHSWESYTPNTLRQATGPQTLLVGAVG
 LRILAQAWKFVGDETYDTIRAEAKNLETHVPSSAAESSLENQSTQEESSNSPEVAHLRS
 VNSDDSTHTGGASNGIQDCDSQLKTVYACLALIGLGTICAMIGLIVYICVLRSLKSSRN
 FSRAQNVKHRNYQRLEYVA"
 gene 128572..131172
 /gene="EHV-1 ORF71"
 CDS 128572..131172
 /gene="EHV-1 ORF71"
 /note="gp2); positional homologue of HSV-1 US5"
 /codon_start=1
 /product="envelope glycoprotein (gp300)"
 /translation="MGFIYARKLLLCMAVSIYAIGSTTTTETTTSSSSSTSGSGQSTSS
 GTTNSSSSPTTSPPTTSSSPPTSTHTSSPSSTSTQSSSTAATSSSAPSTASSTTSIPT
 STSTETTTTTPTASTTTPTTTAAPTAAATTTAVTTAASTSAETTTATATATSTPTTT
 TPTSTTTTTATTTVPTTASTTTDTTTAATTTAATTTAATTTAATTTAATTTAATTTAA
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 TDTTTPSEATTATTSPSTTVSASTTSATTTAFTTESHTSPDSSTGSTSTAEPSTFT
 LTPSTATPSTDQFTGSSASTESDSTDSSTVPTTGTESITESSTTEASTNLGSSTYES
 TEALETDPGNTTSGNTTTPSPSPRTPSFADTQQTPDNGVSTQHTTINDHTTANAQKHAG
 HHRGRAGGRRGSPQGGSHHTPHPDRLTSPDDTYDDDTNHPNGRNNSIEIVPQLPPDR
 PIIELGVATLRKNFMEASCTVETNSGLAIFWKIGNASVDAFNRGTTHTRLMRNGVPVY

ALVSTLRVPWLNVIPLTKITCAACPTNLVAGDGVDLNSCTTKSTTIPCPGQQRTHIFF
 SAKGDRAVCITSELVSQPTITWSVGSDDLRLNDGFSQTWYGIQPGVCGILRSEVRIHRT
 TWRFGSTSKDYLCEVSASDSKTSYKVLNPNHSTSNFALVAATTLTVTILCLLCCLYC
 MLTRPRASVY"
 repeat_region 129121..129270
 /note="6 copies primary repeat unit, 4 copies secondary
 repeat unit: ACGACCACgGCAGCA (7 copies primary repeat
 unit
 in AB4)"
 /rpt_unit=ACGACCACAGCAGCA
 repeat_region 129328..129552
 /note="variable copy number in V592"
 /rpt_unit=ACCACCGCGGCTACC
 gene 131265..132473
 /gene="EHV-1 ORF72"
 CDS 131265..132473
 /gene="EHV-1 ORF72"
 /function="role in virus entry"
 /note="homologous to HSV-1 US6"
 /codon_start=1
 /product="envelope glycoprotein D (gD)"
 /translation="MSTFKLMDGRLVFAMAIAILSVVLSCGTCEKAKRAVRGRQDRP
 KEFPPPRYNYTILTRYNATALASPFINDQVKNDLRIVTATRPCEMIALIAKTNIDSI
 LKELAAAQKTY SARLTWFKIMPTCATPIHDVSYMKNPKLSFAMCDERSDILWQASLI
 TMAAETDDELGLVLAAPAHASAGLYRRVIEIDGRRIYTDFSVTIPSERCPIAFEQNF
 NPDRCKTPEQYSRGEVFTRRFLGEFNFPQGEHMTWLKFWFVYDGGNLPVQFYEAQAF
 RPVPPDNHHPGFDSVESEITQNKTDPKPGQADPKPNQPFKWPSIKHLAPRLDEVDEVIE
 PVTKPPKTSKSNSTFVGISVGLGIAGLVLVGVILYVCLRRKELKKS AQNGLTRLRST
 FKDVKYTQLP"
 gene 132581..133855
 /gene="EHV-1 ORF73"
 CDS 132581..133855
 /gene="EHV-1 ORF73"
 /function="putative Fc receptor, role in envelope
 fusion,
 interacts with gE"
 /note="homologous to HSV-1 US7"
 /codon_start=1
 /product="envelope glycoprotein I (gI)"
 /translation="MAKLTGMFSAAILL SMAICSTAI IYRGEHMSMYLNASSEFAVYP
 TDQSLVLVGHLLFLDGQRLPTTNYSGLIELIHNYSSVCYTVIQTISYESCPRVANNA
 FRSLHKTSKHYHDYFRVNVSVETNVLNITKPQPTDSGAYILRVKLDHAPTADVFGV
 SAFVYDLKSKTVPDPMPTTQTVEPTTSYVSTPTYDYTDDVTTETESTSTSTQQAMTST
 QTPSATWGTQLTTELPTNETVVGIEALLCHWFQPSTRVPTLYLHLLGRTGNLPEDVL
 LVEDSEFLRTTSPAHRPSASPADGDDFKQTNSTSLKARNKIVAMVVIPTACVLMLLLV

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VVGAIINGAVRKHLLSCASRRRIYRSGQGASAAERRRLTCGPTLAASSESLADDTTSS
      gene      PPTPKPSKKTLETDPLMEQLNRKLEAIKEES"
                134088..135740
                /gene="EHV-1 ORF74"
      CDS      134088..135740
                /gene="EHV-1 ORF74"
                /function="putative Fc receptor, role in envelope
fusion,
                interacts with gI"
                /note="homologous to HSV-1 US8"
                /codon_start=1
                /product="envelope glycoprotein E (gE)"

/translation="MELLAASRACIFFGLVTVLDAWGVQQVELSEGAWAMIDGRDVLV
PTNTTTRVTKAWTFLETPPGCAGDISVKKVCVSHSLCEDNIIIGKHCNLLTGEHGIAL
AEFNVVNGSLRRTDDVYFVNGTVFPILAETRSVLQIHRATPSIAGVYTLHVSIDGMMK
HSVVLLTVKKPPKQPQPRLRVKTPPPVTVPVKTHTDFFVHGYHSRVYADGESFEL
SVNLESHIVEPSFSAEIQWYMNNTSSSSCDLFRVFETCFIHPTAMACLHPEQHTCSFT
SPIRATKILHRVYGNCSDHGNSWPSRCHSTLLGNRLYFIQPAQNRVDLLFKDTPASAT
GLYVFFVLLYNHPEAWTYTLLSTANHFMNVLTDVTRPRLGEHFYTDLGHKIITPHPSV
ATTEELGAWTRHYLAFLLVIICTCAALLVALVWGCILYIRSNRKPYEVLNPFETVYT
SVPSNDPSDEVLVFERLASDSDSDSDEELEYPPPKPAPQLPPYQFVDGGDAPS
      gene      GRSGFKVWFRDTPPEASPVPLHKPTLQGPDYSRVASKLKSILK"
                135737..136129
                /gene="EHV-1 ORF75"
      CDS      135737..136129
                /gene="EHV-1 ORF75"
                /note="positional counterpart HSV-1 US8A"
                /codon_start=1
                /product="putative product ORF75"

/translation="MSSNSDNTECFGGVNYAEGMRKRKRNPVRNSTFQEYLDARNARY
PRSGSTSDSDEDYTTTRSKYESDVSEFKKMDLETLPKPAEPQAQKAEPDAAKEEPPVS
      gene      TTSYILNEWVAPMIGHFLAMCMYELLFK"
                136465..137124
                /gene="EHV-1 ORF76"
      CDS      136465..137124
                /gene="EHV-1 ORF76"
                /note="homologous to HSV-1 US9"
                /codon_start=1
                /product="tegument protein"

/translation="MEKAEAAAVVIPLSVSNPSYRSGMSDQEVSEEQSAGDAWVSAA
MAAAEAVAAAATSTGIDNTNDYTYTAASENGDPGFTLGDNITYGPNGAASGCPSPPSPE
VVGLEMVVVSSLAPEIAAAVPADTISASAAAPATRVDDGNAPLLGPGQAQDYDSESGC
YYSESNETASMFIRRVGRQARRHRRRRVALTVAGVILVVVLCAISGIVGAFLARVF
      P"
      CDS      137646..138464

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/ gene="EHV-1 ORF67"
/ note="virulence determinant, identical sequence as
found
in span 124671-123853"
/ codon_start=1
/ product="product of ORF67 (IR6)"

/ translation="MNSDMMTAATAGTEVFRICALARRRRNANPPHLVLAPTFAAAAAGG
AANSSGEEAPRGERKHLFNPFGCMLGRSYFRRCREEMNEGYFAKVPTGYFPVAPSEVP
CRVPVEGVVAGEVLSYSALPLPKIEKRFYKQLNDGTFVRLPFLYPEVYYEGEEEPAD
E
RYYIRADAADASSADPSTLPEEAFKVPPIAIEGITNWQGPRIPIPSERYVMKLGFE
repeat_region 138661..138768
/ note="variable copy number in V592, identical
complementary sequence to span 123549-123656"
/ rpt_unit=CCCCTACCGCTCTCCCCCGCTCGGCCCT
CDS complement(139026..139736)
/ note="homologous to HSV-1 US10, identical sequence as
found in span 122581-123291"
/ codon_start=1
/ product="virion protein"

/ translation="MDGAYGHVHNGSPMAVDGEESGAGTGTGAGADGLYPTSTDAAH
AVSLPRSVGDFAAVVRVSAEAADALRSGAGPPAEAWPRVYRMFCDMFGRYAASPMPV
FHSADPLRRAVGRYLVDLGAAPVETHAELSGRMLFCAYWCCLGHAFACSRPQMYERAC
ARFFETRLGIGETPPADAERYWAALLNMAGAEPELFPRHAAAAAYLRARGRKLPLQLP
CDS SAHRTAKTVAVTGQSINF"
complement(140354..141235)
/ function="putative host range determinant"
/ note="homologous to HSV-1 US1, identical sequence as
found in span 121082-121963"
/ codon_start=1
/ product="putative product of ORF65"

/ translation="MPHQPCGACDGSRCMAQRGTPSTSPLIPSLTPSPAGDPSPRS
SQRIDAVRVPARLPGGSDHPEYGMPLSPRALRPYLARGPGAFCAPPWRPDVNRLAGDV
NRLFRGISTSSIHVTEDSRTLRRALLDFYAMGYTHTRPTLECWQSLQLLPEQSFPLR
ATLRALNSEDRYEQRFLPPSDPPNTLFGEECDVSGDESPSEEEEEDEASGESSVSEF
SPEETASSEYDSFSDVGEDDSSCTGKWSSSESESDSESDAPTNNHHPTTRASAACKR
RKRQPPKGERPTKSARR"
repeat_region 141238..141362
/ note="5 copies in V592 compared with 3 copies in AB4,
identical complementary sequence to span 120955-121079"
/ rpt_unit=CTGGGCCGGGGTCGCCGGAGCTGGG
repeat_region 141434..141503
/ note="10 copies in V592 compared with 16 copies in AB4,
identical complementary sequence to span 120814-120883"
/ rpt_unit=gaccacc
CDS 144019..148482
/ gene="EHV-1 ORF64"
/ note="homologous to HSV-1 RS1, identical sequence as

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found in span 118298-113835"
/codon_start=1
/product="transcriptional regulator"

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/translation="MASQRSDFAPDLYDFIESNDFGEDPLIRAASAAEEGFTQPAAPD
LLYGSQNMFGVDDAPLSTPAVVI PPPSPAPEPRGGKAKRSPSAAGSGGPPTAAAAQP
ASPAPSPAPGLAAMLKMHSSVAPGNRRATGSSSPGGGDAADPVALDSDTETCPGSP
QPEFPSSASPGGGSPAPRVRSISISSSSSSSSSMDEDDQADGAGASSSSSSSSDDSDS
DEGGEEETPRPRHSQNAAKTPSAAGSPGPSSGGDRPAAGAATPKSCRGAASPGAPAP
APASAPAPSRPGGGLLPPGARILEYLEGVREANLAKTLERPEPPAGMASPPGRSPHRL
PKDQRPKSALAGASKRKRRANPRPIPQTQTQAPAE EAPQTAVWDLDMNSSQATGAAA
AASAPAAASCAPGVYQREPLLTSGDPWP GSDPPPMGRVRYGGTGDSRDGLWDDPEIV
LAASRYAEAQAPVPVFPVPEMGDSTKQYNALVRMV FESREAMSWLQNSKLSGQDQNLAQ
FCQKFIHAPRGHSFITGSVANPLPHIGDAMAAGNALWALPHA AASVAMSRRYDRTQK
SFILQSLRRAYADMAYPRDEAGRPDSLAAVAGYPAQAAAAAASQQQPEAPAPSVRVRE
AYTRVCAALGPRRKAAAAAAPGSRAPRPSAFRLRELGDACVLACQAVFEALLRLRGG
ASAVPGLDPSEIPSPACPPEALCSNPAGLETAALS LYE LRD LVERARLLGDSDP THRL
GSDELRLAVRAVLVVARTVAPLVRYNAEGARARASAWTVTQAVFSIPSLVGGMLGEAV
SLLAPPTRSQQPSSSSPGGEPFSGSAAAEGLQTL PPLWPTVPGKQSATVPSSHQSQP
QHSQSGGGAGATTATCCRATQTNARSRGQQHQ PQKARSPQAAASPAHLSQEAMPGSSS
DDRAIHGRPRGKSGKRRSEPLEPAAQAGASASFSSSARGYDPSGPVDSPPAPKRRVAT
PGHQAPRALGMPAEGPDRRGGFRRVPRGDCHTPRPSDAACAAYCPPELVAELIDNQL
FPEAWRPALT FDPQALATIAARCSGPPARDGARFGELAASGPLRRRAAWMHQIPDPED
VKVVVLYSPLQDEDLLGGLPASRPGGSRREPLWSDLKGGLSALLAALGNRILTKRSHA
WAGNWTGAPDVSALNAQGVL LSTGDLAFTGCVEYLC LRLGSARRKLLVLDAVSTEDW
PQDGP AISQYHIYMRAALT PRVACAVRWPRERHLSRAVLTSSTLFGPGLFARAEAAFA
RLYPDSAPLRLCRSSNVAYTV DTRAGERTRVPLAPREYRQRVLPDYDGCKDMRAQAEG
LGFHDPDFEEGAAQSHRAANRWGLGAWLRPVYLACGRRGAGAVEPSELLIPELLSEFC
RVALLEPDAAEAPLVLPI TEAPRRRAPRVDWE PGFGSRSTSVLHMGATELCLPEPDDE
repeat_region LEIDGAGDVELVVEHPGPS PGVAQALRRAPIKIEVVSDDDEDGGDW CNPYLS"
148816..148959
/note="12 copies in V592 compared with 37 in AB4,
identical
complementary sequence to span 113358-113501"
/rpt_unit=GCGGGTTGATGG
repeat_region 148964..149218
/note="identical complementary sequence to span

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113099-113353"
/rpt_unit=TGCTCCTCCCCTTCC
repeat_region 149228..149272
/note="novel repeat not present in AB4, identical
complementary sequence to span 113045-113089"
/rpt_unit=CTACCGCCTACGTCA
misc_feature 149249..149304
/note="56bp insertion compared with

AB4:CCTACGTCACTACCGCCTACGTCATTTCTGCTCCTCCCCTTCCGGTGACGTCA
TT, identical complementary sequence to span
113013-113068"
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SEQUENCE ANNEX 2 - PCR amplification and sequencing primers

Gene	AMPLIFICATION		SEQUENCING	
	Name	Sequence	Name	Sequence
ORF 8	ORF8f	AATTATTGGTGGGCAGAACC	ORF8s	CCATCACCACGCTATTCTC
	ORF8r	TTCTCCAGCACAGCAACG		
ORF11	ORF11f	CTGTAACGATGCTAACGCTACG	ORF11sf1	TAGCCCAAACGACGACAAAG
	ORF11r	TTCAGAAACCTGTCCAGGTCC		
ORF14	ORF14f	CCCCAACTCTAAAACTCG	ORF14s	TTTACACCAATCCACTCC
	ORF14r	AATGTACCATAACACAACCTCC		
ORF15	ORF15f	CAAAGCGCAAAGCAAAATGC	ORF15sf1	ATCCAACACACGCAACATC
	ORF15r	GGGCCTTGATAGTCAGCTCTCC		
ORF30	ORF30f	GCGCTACTTCTGAAAACG	ORF30s	TACCCAAGCATTATCCAG
	ORF30r	CCACAACTTGATAAACACG		
	ORF30f2	AAACCACAAGCCTTACTCC	ORF30s2	GAGAAGACCTTTCAGCGAC
	ORF30r2	GCGCAACTATCACATACG		
ORF33	ORF33f1	TCAAGGAGGAACTAGCTCG	ORF33s1	GTATTCTCCTCGGTTTTTC
	ORF33r1	CCAAAAAGCAACAAACAGG		
	ORF33f2	TTTACGACATCGACAGC	ORF33s2	ACAAAGCCAAAACCTTCCTAC
	ORF33r2	GAGGTCACACTTTGAGTACG		
ORF34	ORF34f	ATTCTCCACGCGGTATCTCC	ORF34s	CGATGTAGACGGACCAGAAG
	ORF34r	ATGTCAAGCGCCATAGAAACG		
ORF37	ORF37f	ACATACTCCGCCATCTCC	ORF37s	CCATCTATAACGCCAGCC
	ORF37r	ACAGCTACATGACTCGTGC		
ORF39	ORF39f	TTACGTACTCAGCGATGG	ORF39s	TAAGAGCACGGATGTAAG
	ORF39r	GGGATAGAAATAGCGAGG		
ORF40	ORF40f	ATCACAAACGCATCCTCG	ORF40s	ACTCGCCGAATCCCAGATG
	ORF40r	CACAGCTCACCCAAAATACC		
ORF52	ORF52f	CCAACAGCTTTCACATCACC	ORF52s	GCTACTTCGTTCACTTCC
	ORF52r	TTCAAATTCTCGCTCACC		
ORF67	ORF67f	CAAAACTCCAACACCACG	ORF67s	GAAGAAGCATTCGCCAAG
	ORF67r	GAGAAGAGGTTCTACAAGCAGC		
ORF68	ORF68f	AGCATTGCCAAACAGTTCC	ORF68s1	GAAGATAGAATGGGTGTGAG
	ORF68r	CAAGAAACCACTGCTCAACC	ORF68s2	AAACCACTGCTCAACCCAC
			ORF68s3	ACCGTTGAGCATAATCATCC
ORF73	ORF73f	GAACATATGAGCATGTACC	ORF73s	ACGGACAACGCTTACCCAC
	ORF73r	GACCAGTAGAACATCTTCC		

SEQUENCE ANNEX 3a -DNA sequence of EHV-1 (strain V592) ORF30

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1   ATGGCGGCGC GCGAACAGGC CAACTCCGTT CGCAGGAGCG GGTTTTTTTAA
51  TCCGTTTATT GGCAAGAGGC CATTTTTTCAG GCCGGGAAGC GGGCAGACCG
101 CGGAGACAGA GCGCCCAAGG CCCCCCAAC ACTCGTACTG CACAGAGGTG
151 GGTAGCTTTA AGTTTATAGC TCCAAGATGC CTCGATGAAG AAGCCCCCGC
201 CGACCAGCGA CGCGGTGTAC ACGTGGGCAC CTTGGAGCGC CCACCCAAAG
251 TGTACTGCGA TGGCTCAGAG TACGACGTGC TGAAC TTTGC CTCCGGAGGT
301 TGCTGGCCTC GCAGGATTCG GTTTGGAAAC GGCCAGGATT TTCGGGGCGA
351 TGGATTCAAC CCCAGATTTG AGAGATTTCA CGTGACGAC ATAGTAGAGA
401 CTTCCGAGAG GCCTCACAC GATGACCCAT CCAGGTTTGC TGAGCTATCC
451 CGCCCAAGCG GGTCTGTGGT AACACTGCTG GGAATGAGCG AGTGTGAAAA
501 GCGAGTCGCG GTTACAGTCT ATGGTGTGCG CCATTATTTT TACATGGCAA
551 AGGCGGAGGT GGATAGCGCT TGTGGAATAA CCACCGAGGC AGAATCGTG
601 CGCGCAATGG TGGACTGCGC GCACAGCTCG GCTTTGAGCG CGGCCCTGGG
651 AAATGGCAAC GGCGGCAAAAC AGAGCGGCGG CAGCGGCGGG GGATGGTGGG
701 GCGGAAAGCA CGTGTCTGCG GACTGCTTCA AAGTGAGAC CGTGTGCCAC
751 ACGACGCTGT ACTACTTTGG ATCTAAGCCA GCTCTCTACT ATAGAGTATC
801 TGCCTCCAGC AGCCGCCTGG GAGGGTTCAT CTGCGACAAC TTTCACCCGG
851 AGATTACAAA ATTCGAGGGG AGCGTGGACG TGACCACGCG GCTGTGTGTG
901 GACAATGAAA ATTTTACCAG TTTTGGGTGG TACCGCCTGC GACCCGCGAC
951 CCACGGAGAG CGTGTTCAAC TTCGCCCCGT TGAGCGACAC GTCACCTCAA
1001 GCGACGTGGA GATTAAC TGT ACTCCGATA ACCTGGAGCC GATACCAGAC
1051 GAGGCTGCCT GGCCCGACTA TAAGCTCATG TGCTTTGATA TAGAGTGTA
1101 AGCTGGAACG GGTAACGAAA TGGCGTTCCC AGTGGCAACT AACCAAGAGG
1151 ACCTGGTCAT CCAGATCTCC TGTCTGCTGT ACTCGCTTGC TACTCAGAAC
1201 CACGAACACA CCCTGCTGTT TTCCCTCGGG TCATGCGATA TCTCTGAGGA
1251 ATACTCGTTT GCATGCGTCC AGCGCGGCGA GCCCAGACCG ACGGTTTTGG
1301 AGTTTGACAG CGAGTACGAG CTGCTGGTTG CTTCTCTGAC CTTTCTCAAG
1351 CAGTACTCTC CCGAGTTTCG CACCGGCTAC AACATCGTTA ATTTTGA CTG
1401 GGCGTACATA GTTAACAAGG TAACGTCGGT GTATAACATC AAGCTGGACG
1451 GGTACGGCAA GTTCAACAAA GGGGGGCTGT TTAAGGTGTG GGACATCGCC
1501 ACGAACCATT TTCAGAAGAA GAGCAAGGTG AAAATCAATG GCCTGATATC
1551 TCTAGACATG TATTCTGTGG CGACGGAAAA GCTAAAGCTA CCCAGCTACA
1601 AACTCGACGC GGTCTGTTGG ACAGTCTCTG GCGAGCATAA GATAGACCTT
1651 CCCTATAAAG AAATACCCTC CTATTACGCG GGAGGGCCTG ACCGGAGGGG
1701 CGTAATAGGA GAGTATTGTA TCCAGGACTC TAGGCTGGTG GGCAAGCTGT
1751 TTTTTAAGTA CCTCCCCCAT CTGGAAC TAT CGGCGGTGGC CAAACTCGCC
1801 CGTATCACCC TAACGCGGGT AATTTTTGAC GGTACAGCAA TTCGCGTGTA
1851 CACGTGCTTG CTGAAACTCG CCCGCGAGAG AAATTTTATT TTGCCAGACA
1901 ACAGACGCCG GTTTGACAGT CAGGCAGACG CCGCGTCAGA GACTTCGGAG
1951 TTGGCTATGG ATAGCCAAAG CCACGCCTTC GACAGTACAG ACGAACCCGA
2001 CGGTGTGGAC GGTACCCCGG ACGCCGACAG ATCTGGCGCT ACTTCTGAAA
2051 ACGGAGGCGG GAAGCCCGGC TCGGGGAGGG CCGTGGGCTA CCAGGGAGCA
2101 AAGGTTCTAG ACCCCGTATC CGGCTTTTCA GTGGACCCCG TGGTTGTGTT
2151 TGACTTCGCT AGCTTATACC CAAGCATTAT CCAGGCCCAT AACCTCTGTT
2201 TCACCACCTT GCGCTCGAT GAAGTGGATC TGGCCGGGCT TCAACCATCC
2251 GTCAACTACT CGACGTTTCA GGTGGGTGAC CAAAAGTTAT TTTTGTCCA
2301 CGCCCATATT CGCGAAAGCC TGCTTGGCAT CTTGCTGCGC GACTGGCTGG
2351 CCATGCGAAA GGCGGTGAGG GCGCGAATCC CCACCAGCAC CCCCAGGAG
2401 GCAGTTTTAC TAGATAAGCA GCAGTCTGCG ATTAAGGTGA TATGCAACTC
2451 GGTTTACGGA TTCACGGGGG TGGCAAACGG CCTGTTGCCG TGTCTGAGGA
2501 TAGCGGCTAC CGTTACCACG ATAGGACGCG ACATGCTCCT CAAGACCCGA
2551 GATTACGTTT ACTCTCGTTG GGCGACGCGC GAGCTGCTGG AGGACAATTT
2601 TCCAGGGGCT ATAGGTTTCC GAAACCACAA GCCTTACTCC GTCAGGGTTA
2651 TCTACGGAGA CACCGACTCC GTGTTTATCA AGTTTGTGGG CCTGACGTAC
2701 GAGGGGGTAT CGGAGCTGGG GGATGCTATG TCGCGTCAGA TTTCAGCGGA
2751 CCTCTTTAGA GCGCCCATCA AACTGGAGTG TGAGAAGACC TTTCAGCGAC
2801 TGCTGCTGAT CACCAAGAAG AAGTACATAG GTGTCATAAA CGGGGGGAAG
2851 ATGCTCATGA AGGGGGTCTG CCTGGTCCGC AAAAATAACT GCTCTTTCAT
2901 AAATTGTGAC GCGCGACATC TGGTAGATCT TTTGTTGTAC GACGAGGATG

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2951 TGGCCACGGC GGCAGCAAAG GTGACAGACG TGCCTCCCGC AGAATGGGTG
3001 GGGCGCCCGC TACCGAGCGG CTTTGACAAG TTTGGGCGAG TGCTGGTAGA
3051 GGCGTACAAC CGTATCACTG CCCCCAACTT GGACGTGCGC GAGTTCGTTA
3101 TGA CTGCTGA GCTGAGCCGC TCACCCGAAT CGTATACCAA CAAGCGCCTG
3151 CCGCACCTCA CCGTCTACTT TAAGCTCGCC ATGAGGAATG AAGAACTGCC
3201 CAGCGTAAAA GAGAGAATTC CGTATGTGAT AGTTGCGCAG ACCGAGGCCG
3251 CGGAACGCGA AGCGGGTGTA GTAAACTCAA TGC GCGGTAC CGCCAAAAC
3301 CCCGTGGTAA CCAAGACCGC ACGCCCCCAA CCTAAACGCA AACTGCTGGT
3351 TTCCGACCTC GCCGAAGACC CGACCTATGT TTCCGAGAAT GACGTACCGC
3401 TAAACACAGA CTACTATTTT TCCCACCTGT TGGGTACCAT AAGCGTGACC
3451 TTTAAGGCTC TATTCGGAAA TGATGTGAGA ACAACAGAAA ATCTTTTAAA
3501 GCGGTTTATT CCGGAAACCC CCCACAAGAC CCCCACGAAA ACCCAGGCAC
3551 TGCTTGAGCG CGCCGGCTTT GAAAAGCTGA CGCCCTTTAC ACCGGAGGAA
3601 GAAAGTCGTC GAATACTGCA TACAGTTTTT TGTACTCTAG AAGCAGCTCC
3651 CCATCAAAGC TGA

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SEQUENCE ANNEX 3b - Amino acid sequence of EHV-1 (strain V592) ORF30

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1   MAAREQANSV RRSGLFNPFI GKRPFFRPGS GQTAETERPR PPQHSYCTEV
51  GSFKFIAPRC LDEEAPADQR RGVHVGTLER PPKVYCDGSE YDVLNFAASGG
101 CWPRRIRVWN GQDFRGDGFN PRFERFHVYD IVETSESASH DDPSRFAELS
151 RPSGSSVVTLL GMSECGKRVA VHVYGVRYHYF YMAKAEVDSA CGITTEAELV
201 RAMVDCAHSS ALSAALGNNG GKGQSGGSGG GWWGGKHVSA DCFKVETVCH
251 TTLYYFGSKP ALYYRVSASS SRLGGFICDN FHPEITKFEG SVDVTTRLLL
301 DNENFTSFGW YRLRPGTHGE RVQLRPVERH VTSSDVEINC TPDNLEPIPD
351 EAAWPDYKLM CDFIECKAGT GNEMAFPVAT NQEDLVIQIS CLLYSLATQN
401 HEHTLLFSLG SCDISEEYSF ACVQRGEPRP TVLEFDSEYE LLVAFITFLK
451 QYSPEFATGY NIVNFDWAYI VNKVTSVYNI KLDGYGKFNK GGLFKVWDIA
501 TNHFQKKSKV KINGLISLDM YSVATEKLKL PSYKLDVAVG DVLGEHKIDL
551 PYKEIPSYYA GGPDRRGVIG EYCIQDSRLV GKLEFFKYLPH LELSAVAKLA
601 RITLTRVIFD GQQIRVYTCL LKLARERNFI LPDNRRRFD$ QADAASETSE
651 LAMDSQSHAF DSTDEPDGVD GTPDAAGSGA TSENGGGKPG VGRAVGYQGA
701 KVLDPVSGFH VDPVVVFDFA SLYPSIIQAH NLCFTTLALD EVDLAGLQPS
751 VNYSTFEVGD QKLFFVHAHI RESLLGILLR DWLAMRKAVR ARIPTSTPEE
801 AVLLDKQQSA IKVICNSVYG FTGVANGLLP CLRIAATVTT IGRDMLLKTR
851 DYVHSRWATR ELLEDNFPGA IGFRNHKPYS VRVIYGDTS VFIKRVGLTY
901 EGVSELGDAM SRQISADLFR APIKLECEKT FQRLLLITKK KYIGVINGGK
951 MLMKGVDLVR KNNCSFINLY ARHLVDLLLY DEDVATAAAK VTDVPPAEWV
1001 GRPLPSGFDK FGRVLVEAYN RITAPNLDVR EFVMTAELSR SPESYTNKRL
1051 PHLTVYFKLA MRNEELPSVK ERIPYVIVAQ TEAAEREAGV VNSMRGTAQN
1101 PVVTKTARPQ PKRKLLVSDL AEDPTYVSEN DVPLNTDYYF SHLLGTISVT
1151 FKALFGNDVR TTENLLKRFI PETPHKTPTK TQALLERAGF EKLTPFTPEE
1201 ESRRILHTVF CTLEAAPHQS

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Figure 1. Multi-locus sequence analysis

Outbreak	ORF marker region																Disease
	68	8	11	14	15	30-m1	30-m2	33-m1	33-m2	34	37	39	40	52	67	73	
GB83/1/1	1	1	1	1	1	2	1	1	1	1	1A	1	1	1	1*	1	Non-paralytic
GB83/3/1	1	1	-	1B	-	2	1	1	1	1	1A	1	1	1	1*	-	
GB86/1/1	1	1	1	2	1	2	1	1	1	1	1A	2	1	1	1*	1	
US85/1/1	1A	-	1	1	1	2	1	1	1	1	-	1	1	1	1	1	
GB80/1/2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	Paralytic
GB93/4/2	1*	1	1	1	1	1	1	1	1	1	1A	1	1	1	1*	-	
GB81/4/1	2A	1	1	1	1	2	1	1	1	1	1A	1	1	1	1*	-	Non-paralytic
GB86/2/1	2	1	-	1	-	2	1	1	1	1	1A	1	1	1	1*	-	
US76/1/1	2	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	
US79/1/1	2	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	
US83/1/1	2	-	-	1	-	2	1	1	1	1	-	-	-	-	-	-	Paralytic
US83/2/1	2	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	
US84/1/1	2	-	-	2	-	2	1	1	1	1	-	-	-	-	-	-	
US99/1/1	2	-	1	2	2	2	1	2	2	2A	2	2	1	-	1	1	
US00/1/1	2	-	-	2	-	2	1	1	1	1	-	-	-	-	-	-	Paralytic
GB93/5/2	2*	1	-	-	-	-	-	-	-	-	1A	-	-	-	-	-	
GB99/1/2	2	-	1	-	2	1	-	-	2	-	-	2	-	-	-	-	
GB02/2/2	2	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	
GB03/2/2	2	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	Non-paralytic
US70/1/2	2	-	1	1A	1	1	1	1	2	1	1A	1	1	1	-	1	
US85/2/2	2	-	1	2	-	2	1	1	1	1	1A	1	1	1	1	1	
US86/2/2	2	-	-	2	-	1	-	1	1	1	-	-	-	-	-	-	
US86/3/2	2	-	1	2	1	1	1	1	1	1	-	-	-	-	-	-	Non-paralytic
GB81/1/1	3	-	1	1	-	2	1	1	1	1	1A	2	1	1	1	1	
GB83/2/1	3*	1	-	2A	-	2	-	2	2	1*	2	2	1	2	1*	-	
GB85/2/1	3*	1	-	-	-	-	1	2	2	1*	2	2	-	-	-	1*	
GB88/1/1	3*	1	-	2A	-	2	1	2	2	1	2	2	1	2	-	-	Paralytic
GB89/1/1	3A	1	1	2A	2	2	1	2	2	1	2	2	1	2	1*	1	
GB89/2/1	3A	1	-	2A	-	2	-	2	2	1*	2	2	1	2	1*	-	
GB89/3/1	3*	1	-	2A	-	2	1	2	2	1*	2	2	1	2	1*	-	
GB91/2/1	3	1	-	-	-	2	1	2	2	1	2	2	1	2	1*	-	Paralytic
GB93/1/1	3*	-	-	-	-	2	1	-	-	-	-	2	-	-	-	-	
GB93/2/1	3*	1	-	2A	-	2	1	2	2	-	2	2	1	2	1*	-	
GB93/3/1	3*	1	-	2A	-	2	1	2	2	1*	2	2	1	2	1*	-	
GB00/2/1	3	-	-	-	-	2	-	-	2	-	-	2	-	2	-	-	Paralytic
GB01/1/1	3	-	-	2A	-	2	1	2	2	-	-	2	1	2	1*	-	
GB02/1/1	3	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	
US86/1/1	3	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	
GB88/2/2	3	1	1	2	2	1	1	2	2	1	2	2	1	2	1	1	Non-paralytic
GB03/3/2	3	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	
GB03/4/2	3	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	
GB81/2/1	4	1	1	2	2	2	1	2	2	1	2	2	1	2	1	-	
GB81/3/1	4	-	1	2A	2	2	1	2	2	1/2*	2	2	1	2	1*	1	Paralytic
GB00/1/1	4A	-	1	2A	2	2	1	2	2	1/2*	2	2	1	2	1	-	
GB80/2/2	4*	-	-	-	-	1	1	2	2	1	-	2	-	-	-	-	
GB86/3/2	4B	1	1	-	2	2	1	2	2	1	2	2	1	2	1	-	
US86/4/2	4	-	1	2A	2	1	1	2	2	2B	2	2	1	2	1*	1	Attenuated
PL68/1/0	5	1	-	3	-	1A	-	-	-	1	2	-	-	-	-	-	
US72/1/0	5	-	-	2*	-	1	-	2	2	2	-	-	-	-	-	-	
US75/1/1	5	-	1	2*	2	2	1	2	2	2A	2	2	1	2	-	1	
US81/1/1	5	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	Paralytic
US41/1/2	5	1	-	2B	-	1	-	-	-	2	2	-	-	-	-	-	
US79/2/2	5	-	-	-	2	1	1	2	2	2A	-	-	-	-	-	-	
US82/1/2	5	-	-	2*	-	1	1	2	2	2B	-	-	-	-	-	-	
US83/3/2	5	-	-	2*	-	1	1	2	2	2	-	-	-	-	-	-	Non-paralytic
US99/2/2	5	-	1	2*	2	1	1	2	1	1	2	2	1	2	1A	1	
US99/3/2	5	-	1	2*	2	2B	1	2	2	2A	2	2	1	2	1A	1	
US01/1/2	5	-	-	-	-	1	1	2	2	2	-	-	-	-	-	-	
US02/1/2	5	-	1	2	-	2B	1	2	2	1/2*	2	2	1	2	1A	1	Non-paralytic
GB85/1/1	6	2	2	2	2	2	2	2	2	3	2	3	2	2	2	2	
GB91/1/1	6*	2	2	2A	2	2	2	2	2	3	2	3	2	2	2*	2	
GB00/3/1	6*	-	-	2	-	2A	2	2	2	-	-	3	2	2	2*	-	
GB01/2/1	6	-	2	2	2	2A	2	2	2	3*	2	3	2	2	2*	2	